



SEQUENCE LISTING

<110> Wands, Jack R.
de la Monte, Suzanne M.
Ince, Nedim
Carlson, Rolf I.

<120> DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

<130> 21486-032 DIV3

<140> 09/903,063
<141> 2001-07-11

<150> 09/436,184
<151> 1999-11-08

<160> 9

<170> PatentIn Ver. 2.1

<210> 1
<211> 36
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Consensus
EGF-like domain

<220>
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<222> (2)..(8)
<223> Wherein Xaa is any amino acid

<220>
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<220>
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<220>
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<220>

<221> VARIANT

<222> (28)..(35)

<223> Wherein Xaa is any amino acid.

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1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Cys
35

<210> 2

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2

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Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
35 40 45

Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
50 55 60

Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
65 70 75 80

Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
85 90 95

Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
100 105 110

Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
115 120 125

Glu Pro Glu Glu Gln Val	Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
130	135 140
Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His	
145	150 155 160
Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr	
165	170 175
Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val	
180	185 190
Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr	
195	200 205
Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln	
210	215 220
Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu	
225	230 235 240
Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr	
245	250 255
Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu	
260	265 270
Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val	
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Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu	
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Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro	
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Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys	
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Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg	
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Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val	
355	360 365
Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys	
370	375 380

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Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg			
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Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala			
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Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp			
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675 680 685

Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys
690 695 700

Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp
705 710 715 720

Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu
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Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg
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Arg Ser Leu Pro Ala Ile
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<211> 2324

<212> DNA

<213> Homo sapiens

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<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-like
cysteine-rich repeat

<220>

<221> VARIANT

<222> (3)..(5)

<223> Wherein any Xaa may be any amino acid

<220>

<221> VARIANT

<222> (6)..(7)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (10)

<223> Wherein Xaa is any amino acid.

<220>
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<220>
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 <222> (17)..(18)

<220>
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<220>
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 <212> PRT
 <213> Homo sapiens

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 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
 35 40 45
 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
 50 55 60
 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
 65 70 75 80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
 85 90 95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
 100 105 110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly
 115 120 125

Ala Gly Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
 130 135 140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
 145 150 155 160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
 165 170 175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
 180 185 190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu
 195 200 205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu
 210 215 220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
 225 230 235 240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
 245 250 255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
 260 265 270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
 275 280 285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
 290 295 300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
 305 310 315 320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
 325 330 335

Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn
 340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
 355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
 370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Thr Ser Gly His
 385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
 405 410 415

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly
 420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp
 435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Glu Leu Ser Asn
 450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn
 465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro
 485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala
 500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala
 515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser
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Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro
 545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe
 565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu
 580 585 590

Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr
 595 600 605
 Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser
 610 615 620
 Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val
 625 630 635 640
 Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg
 645 650 655
 Val Asp Pro Asn Gly Tyr Met Met Met Ser Pro Ser Gly Gly Cys Ser
 660 665 670
 Pro Asp Ile Gly Gly Gly Pro Ser Ser Ser Ser Ser Ser Ser Asn Ala
 675 680 685
 Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly
 690 695 700
 Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser
 705 710 715 720
 Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser
 725 730 735
 Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly
 740 745 750
 Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro
 755 760 765
 Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala
 770 775 780
 Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr
 785 790 795 800
 Ala Ala Thr Ala Asp Asp Ser Ser Ser Ser Thr Ser Ser Asp Ser Leu
 805 810 815
 Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro
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 His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala
 835 840 845

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Gln Gln Pro Leu Leu His	Pro Pro Glu Pro Lys Ser	Pro Gly Glu Tyr
885	890	895
Val Asn Ile Glu Phe Gly	Ser Asp Gln Ser Gly Tyr	Leu Ser Gly Pro
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Val Ala Phe His Ser Ser	Pro Ser Val Arg Cys Pro	Ser Gln Leu Gln
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Pro Ala Pro Arg Glu Glu	Glu Thr Gly Thr Glu Glu	Tyr Met Lys Met
930	935	940
Asp Leu Gly Pro Gly Arg	Arg Ala Ala Trp Gln	Glu Ser Thr Gly Val
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Glu Met Gly Arg Leu Gly	Pro Ala Pro Pro Gly	Ala Ala Ser Ile Cys
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980	985	990
Gln Met Ser Cys Pro Arg	Gln Ser Tyr Val Asp	Thr Ser Pro Ala Ala
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Pro Val Ser Tyr Ala Asp	Met Arg Thr Gly Ile	Ala Ala Glu Glu Val
1010	1015	1020
Ser Leu Pro Arg Ala Thr	Met Ala Ala Ala Ser	Ser Ser Ser Ala Ala
1025	1030	1035 1040
Ser Ala Ser Pro Thr Gly	Pro Gln Gly Ala Ala	Glu Leu Ala Ala His
1045	1050	1055
Ser Ser Leu Leu Gly Gly	Pro Gln Gly Pro Gly	Gly Met Ser Ala Phe
1060	1065	1070
Thr Arg Val Asn Leu Ser	Pro Asn Arg Asn Gln	Ser Ala Lys Val Ile
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Arg Ala Asp Pro Gln Gly	Cys Arg Arg Arg His	Ser Ser Glu Thr Phe
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Ser Ser Thr Pro Ser Ala Thr Arg Val Gly Asn Thr Val Pro Phe Gly
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Ala Gly Ala Ala Val Gly Gly Gly Gly Ser Ser Ser Ser Ser Glu
1125 1130 1135

Asp Val Lys Arg His Ser Ser Ala Ser Phe Glu Asn Val Trp Leu Arg
1140 1145 1150

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1155 1160 1165

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1170 1175 1180

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<212> DNA
<213> Homo sapiens

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